AMENDMENTS

In the claims:

Please amend the claims as follows.

Claims 1-14 (canceled).

15. (withdrawn) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand comprises a common ligand, wherein said common ligand competes for cofactor binding to an enzyme in said enzyme family, and a first specificity ligand, wherein said specificity ligand binds to a substrate binding site of said first enzyme;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a second specificity ligand, wherein said specificity ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said first specificity ligand and said second specificity ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

16. (withdrawn) The method of claim 15, wherein said enzyme family is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

17. (withdrawn) The method of claim 15, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

18. (withdrawn) The method of claim 15, wherein said common ligand and said specificity ligands are attached by a linker having approximate C2 symmetry.

19. (withdrawn) The method of claim 18, wherein said linker has perfect C2 symmetry.

Claims 20-36 (canceled).

37. (withdrawn) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand

comprises a common ligand, wherein said common ligand competes for cofactor binding to an enzyme in an enzyme family, and a first specificity ligand, wherein said specificity ligand binds to a substrate binding site of said first enzyme, wherein said enzyme family comprises two or more enzymes that bind to the same cofactor;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a second specificity ligand, wherein said specificity ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said first specificity ligand and said second specificity ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

38. (withdrawn) The method of claim 37, wherein said enzyme family is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

39. (withdrawn) The method of claim 37, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin

mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

40. (withdrawn) The method of claim 37, wherein said common ligand and said specificity ligands are attached by a linker having approximate C2 symmetry.

41. (withdrawn) The method of claim 40, wherein said linker has perfect C2 symmetry.

42. (currently amended) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family by: [, wherein said bi-ligand comprises a common ligand, wherein said common ligand is a cofactor or mimic thereof, and a second ligand, wherein said second ligand binds to a substrate binding site of said first enzyme;]

(a)(i) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of an enzyme in said enzyme family, to form a module;

(a)(ii) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(a)(iii) screening said population of bi-ligands for binding to an enzyme in said enzyme family;

(a)(iv) identifying a bi-ligand that binds to and has specificity for said enzyme;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family by repeating steps (a)(iii) and (a)(iv) to identify a bi-ligand that binds to and has specificity for a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third ligand, wherein said common ligand, said second ligand and said third ligand are attached to said linker so that said common ligand and said second ligand can bind to said first enzyme and said common ligand and said third ligand can bind to said second enzyme, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

43. (original) The method of claim 42, wherein said enzyme is selected from the group consisting of

kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

44. (original) The method of claim 42, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

45. (original) The method of claim 42, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

46. (original) The method of claim 45, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.

47. (currently amended) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand comprises a common ligand[, wherein said common ligand is a

cofactor or mimic thereof,] and a second ligand, [wherein said second ligand binds to a substrate binding site of said first enzyme,] wherein said enzyme family comprises two or more enzymes that bind to the same cofactor, by: [;]

(a)(i) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of an enzyme in said enzyme family, to form a module;

(a)(ii) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(a)(iii) screening said population of bi-ligands for binding to an enzyme in said enzyme family;

(a)(iv) identifying a bi-ligand that binds to and has specificity for said enzyme;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family by repeating steps (a)(iii) and (a)(iv) to identify a bi-ligand that binds to and has specificity for a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third ligand, wherein said common ligand, said second ligand and said third ligand are attached to said linker so that said common ligand and said second ligand can bind to said first enzyme and said common ligand and said third ligand can bind to said second enzyme, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

(a) attaching a linker to a common ligand, wherein said common ligand is a cofactor or mimic thereof and wherein said linker has sufficient length and orientation to direct a second ligand to a substrate binding site of an enzyme in said enzyme family, to form a module;

(b) generating a population of bi-ligands, wherein said bi-ligand comprises said module and a second ligand linked by said linker;

(c) screening said population of bi-ligands for binding to an enzyme in said enzyme family;

(d) identifying a bi-ligand that binds to and has specificity for said enzyme; and

(e) repeating steps (c) and (d) to identify a bi-ligand that binds to and has specificity for a second enzyme in said enzyme family.

48. (original) The method of claim 47, wherein said enzyme is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

49. (original) The method of claim 47, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

50. (original) The method of claim 47, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

51. (original) The method of claim 50, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.

52. (original) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand

comprises a common ligand, wherein said common ligand binds to a cofactor binding site, and a second ligand, wherein said second ligand binds to a substrate binding site of said first enzyme;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

53. (original) The method of claim 52, wherein said enzyme is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

54. (original) The method of claim 52, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A,

tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

55. (original) The method of claim 52, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

56. (original) The method of claim 55, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.

57. (withdrawn) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand comprises a common ligand, wherein said common ligand binds to a cofactor binding site and competes for cofactor binding, and a second ligand, wherein said second ligand binds to a substrate binding site of said first enzyme;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third

ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

58. (withdrawn) The method of claim 57, wherein said is enzyme selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α-ketodecarboxylases.

59. (withdrawn) The method of claim 57, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

60. (withdrawn) The method of claim 57, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

61. (withdrawn) The method of claim 60, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.